Amendments to the Specification:

Please replace the paragraph beginning at page 4, line 13, with the following amended paragraph:

Figure 1 shows the amino acid sequence (SEQ ID NO:4) of the reproductive peptide PrAG1, together with the nucleotide sequence coding therefor (SEQ ID NO:3);

Replace the paragraph beginning at page 4, line 19, with the following amended paragraph:

Figure 2 shows the sequence of the PrAG1 promoter, which is the focus of the present invention, isolated from *Pinus radiata* (SEQ ID NO:2);

Replace the paragraph beginning at page 4, line 30, with the following amended paragraph:

Figure 5 is a Reverse Transcription-Polymerase Chain Reaction (RT-PCR) analysis showing reproductive-organ specific expression of PrAG1. RT-PCR analysis was performed on total RNA isolated from different organs of radiata Pine: (M) immature male cone, (F) immature female cone, (Vs) vegetative shoot, (N) needle and (S) stem. MADS ~~mads~~ box genes were amplified with PrAG1 gene-specific oligonucleotides. Products from the PCR reactions were electrophoresed, blotted, and hybridized with a labelled probe of PrAG1 specific fragment;

Replace the paragraph beginning at page 17, line 29, with the following amended paragraph:

6) The 1105 bp and 449 bp fragments were used in PCR mediated DNA splicing to synthesize one continuous 1458 pb promoter fragment of PrAG1. This was done as described. One primer was synthesized based on the 5'end sequence of 1105 bp

promoter fragment: Primer PLi, 5' AGT TAC TTA ACA ATG CGC AAC CAA GGC 3' (SEQ ID NO.~~12~~ 13). Primer pair PLi and GSP2 was used in PCR to get the promoter fragment of 1105 pb, in which the AP2 primer sequence was removed. This 1105 bp fragment and 449 bp fragment was then added in one PCR tube as a template with the primer pair of AP2 and GAP2 to do the second round PCR to get the 1458 bp PCR fragment. The conditions of second round PCR were as follows: the first cycle at 95°C for 5 minutes, and 68°C for 10 min; the second cycle at 94°C for 30 seconds (DNA denaturing), DNA annealing at 60°C for 1 min, and DNA synthesis at 72°C for 2 minutes; this regime was cycled 30 times. This 1458 bp fragment was then cloned into pGEM-T easy vector (Promega) and subjected to DNA sequencing on both strands to confirm the DNA sequence and to make sure that no base changes occurred during the PCR process.

Replace the paragraph beginning at page 20, line 20, with the following amended paragraph:

A DNA fragment containing the PrAG1 promoter (1.40 kb, SEQ ID NO:2) ~~1.46 kb, sequence of Figure 2)~~ operably fused to an RNAse gene (0.95 kb, RNS2, Taylor *et al. Proc Natl Acad Sci,* USA 90 (11), 5118-5122 (1993)) and containing Hind III and Sac I sites was gel purified and ligated into the Hind III/Sac I sites of binary vector pRD420, containing the NPTII gene for plant selection, (provided by Dr. R.S.S. Datla, PBI, Saskatoon, Canada) resulting in the construct pRAGPR (Figure 6). The construct was introduced into *Agrobacterium tumefaciens* (strain c58 MP90), and used to transform and regenerate *Nicotiana tabacum* var. *Xanthi* by the standard leaf disc transformation ethod (Horsch *et al.* (1985), A simple and general method for transferring genes into plants. *Science* 227, 1229-1231). Control lines were also generated through leaf disk method without the selection process. After kanamycin selection, the putative transgenic plantlets were rooted in the rooting medium containing kanamycin and then moved to pots containing the Metromix 350 potting mix. Potted plants were maintained under controlled conditions in a growth chamber with 16h photoperiod. The plants were grown through the full life cycle of

the tobacco until senescence and the flowering of the transgenic tobacco assessed relative to controls. Transgenic plants were identified further by PCR with template of genomic DNA and Southern blot analysis to confirm the integration of pRAGPR in transgenic tobacco plants.

Insert an Abstract paragraph on new page 28. The Abstract is presented here on the following separate page: